Figure 1

```
   1 CCGGTGCCAG CCCAGGTGCT CGCGGCCTGG CTCCATGGCC CTGGTCACAG TGAGCCGTTC
  61 GCCCCCGGGC AGCGGCGCCT CCACGCCCGT GGGGCCCTGG GACCAGGCGG TCCAGCGAAG
 121 GAGTCGACTC CAGCGAAGGC AGAGCTTTGC GGTGCTCCGT GGGGCTGTCC TGGGACTGCA
 181 GGATGGAGGG GACAATGATG ATGCAGCAGA GGCCAGTTCT GAGCCAACAG AGAAGGCCCC
 241 GAGTGAGGAG GAGCTCCACG GGGACCAGAC AGACTTCGGG CAAGGATCCC AGAGTCCCCA
 301 GAAGCAGGAG GAGCAGAGGC AGCACCTGCA CCTCATGGTA CAGCTGCTGA GGCCGCAGGA
 361 TGACATCCGC CTGGCAGCCC AGCTGGAGGC ACCCCGGCCT CCCCGGCTCC GCTACCTGCT
 421 GGTAGTTTCT ACACGAGAAG GAGAAGGTCT GAGCCAGGAT GAGACGGTCC TCCTGGGCGT
 481 GGATTTCCCT GACAGCAGCT CCCCCAGCTG CACCCTGGGC CTGGTCTTGC CCCTCTGGAG
 541 TGACACCCAG GTGTACTTAG ATGGAGACGG GGGCTTCAGC GTGACGTCTG GTGGGCAAAG
 601 CCGGATCTTC AAGCCCATCT CCATCCAGAC CATGTGGGCC ACACTCCAGG TATTGCACCA
 661 AGCATGTGAG GCAGCTCTAG GCAGCGGCCT TGTACCGGGT GGCAGTGCCC TCACCTGGGC
 721 CAGCCACTAC CAGGAGAGAC TGAACTCCGA ACAGAGCTGC CTCAATGAGT GGACGGCTAT
 781 GGCCGACCTG GAGTCTCTGC GGCCTCCCAG CGCCGAGCCT GGCGGGTCCT CAGAACAGGA
 841 GCAGATGGAG CAGGCGATCC GTGCTGAGCT GTGGAAAGTG TTGGATGTCA GTGACCTGGA
 901 GAGTGTCACT TCCAAAGAGA TCCGCCAGGC TCTGGAGCTG CGCCTGGGGC TCCCCCTCCA
 961 GCAGTACCGT GACTTCATCG ACAACCAGAT GCTGCTGCTG GTGGCACAGC GGGACCGAGC
1021 CTCCCGCATC TTCCCCCACC TCTACCTGGG CTCAGAGTGG AACGCAGCAA ACCTGGAGGA
1081 GCTGCAGAGG AACAGGGTCA CCCACATCTT GAACATGGCC CGGGAGATTG ACAACTTCTA
1141 CCCTGAGCGC TTCACCTACC ACAATGTGCG CCTCTGGGAT GAGGAGTCGG CCCAGCTGCT
1201 GCCGCACTGG AAGGAGACGC ACCGCTTCAT TGAGGCTGCA AGAGCACAGG GCACCCACGT
1261 GCTGGTCCAC TGCAAGATGG GCGTCAGCCG CTCAGCGGCC ACAGTGCTGG CCTATGCCAT
1321 GAAGCAGTAC GAATGCAGCC TGGAGCAGGC CCTGCGCCAC GTGCAGGAGC TCCGGCCCAT
1381 CGCCCGCCCC AACCCTGGCT TCCTGCGCCA GCTGCAGATC TACCAGGGCA TCCTGACGGC
1441 CAGCCGCCAG AGCCATGTCT GGGAGCAGAA AGTGGGTGGG GTCTCCCCAG AGGAGCACCC
1501 AGCCCCTGAA GTCTCTACAC CATTCCCACC TCTTCCGCCA GAACCTGAGG GTGGTGGGGA
1561 GGAGAAGGTT GTAGGCATGG AAGAGAGCCA GGCAGCCCCG AAAGAAGAGC CTGGGCCACG
1621 GCCACGTATA AACCTCCGAG GGGTCATGAG GTCCATCAGT CTTCTGGAGC CCTCCTTGGA
1681 GCTGGAGAGC ACCTCAGAGA CCAGTGACAT GCCAGAGGTC TTCTCTTCCC ACGAGTCTTC
1741 ACATGAAGAG CCTCTGCAGC CCTTCCCACA GCTTGCAAGG ACCAAGGGAG GCCAGCAGGT
1801 GGACAGGGGG CCTCAGCCTG CCCTGAAGTC CCGCCAGTCA GTGGTTACCC TCCAGGGCAG
1861 TGCCGTGGTG GCCAACCGGA CCCAGGCCTT CCAGGAGCAG GAGCAGGGGC AGGGGCAGGG
1921 GCAGGGAGAG CCCTGCATTT CCTCTACGCC CAGGTTCCGG AAGGTGGTGA GACAGGCCAG
1981 CGTGCATGAC AGTGGAGAGG AGGGCGAGGC CTGAGCCCTC ACACATGCCC ACGCTCCCCT
2041 GACACTGAAG AGGATCCACA ACTCCTTGGA GAAACACCCT CACGTCTGTT GCCGCACACA
2101 TTCCTCTCAG CTCCGCCCCA TACCCGTCAC TACAGCCTCA CCTCCCACCC CTGTCACTAC
2161 GGCCTCACCT CCCACCCCTG TCACTACAGC CTCACCTCCT ACAGCCTTAA GTCCCAGGCC
2221 CATGTCTGCC TGTCCAAGGG CTCAAGACTT TCTAACTGGG ATGTGGTAGA GGGACTGAAG
2281 GTACCTTTGG GGGCAACAGC ACCCTAGTTT CATTCTCAAC TCTAGCCCTG CACACTCACC
2341 TGTGGCACGG AATGAAAACA GAGCTTCCCG TGCAAAAAGG GTCACGCCTC CCACCCCCGC
2401 CCCCTCCCTG CACCTCCTGT CCTCTCCCAG TTCATTCCTG GAACCAGCCA GGCCAGGCAA
2461 CCAGTGGCCC CCAAAGGCAG GCAGGATCCT CAGGCCCCAG CCGCGGGAGG CTGGAAGGGC
2521 TGGCAGATCG CTTCCCTCAT CCACCTCCAC CGGTCCAGGT CTTTGCTGCT GTCCCCAGAC
2581 CTCCTGTGAC ACCACGCCAG ATCACAGGGC ACCAGGCCAG AGATAGTCTT CTTTTTGTCC
2641 TTTCTGGCCT CTGGCTAGTC AGTTTTTCAT AGCCTTACAG TATCTGGCTT TGTACTGAGA
2701 AATAAAACAC ATTTTCAT
```

Figure 2

```
MALVTVSRSPPGSGASTPVGPWDQAVQRRSRLQRRQSFAVLRGAVLGLQDGGDNDDAAEASSEPTEKAPSEEELHGD
QTDFGQGSQSPQKQEEQRQHLHLMVQLLRPQDDIRLAAQLEAPRPPRLRYLLVVSTREGEGLSQDETVLLGVDFPDS
SSPSCTLGLVLPLWSDTQVYLDGDGGFSVTSGGQSRIFKPISIQTMWATLQVLHQACEAALGSGLVPGGSALTWASH
YQERLNSEQSCLNEWTAMADLESLRPPSAEPGGSSEQEQMEQAIRAELWKVLDVSDLESVTSKEIRQALELRLGLPL
QQYRDFIDNQMLLLVAQRDRASRIFPHLYLGSEWNAANLEELQRNRVTHILNMAREIDNFYPERFTYHNVRLWDEES
AQLLPHWKETHRFIEAARAQGTHVLVHCKMGVSRSAATVLAYAMKQYECSLEQALRHVQELRPIARPNPGFLRQLQI
YQGILTASRQSHVWEQKVGGVSPEEHPAPEVSTPFPPLPPEPEGGGEEKVVGMEESQAAPKEEPGPRPRINLRGVMR
SISLLEPSLELESTSETSDMPEVFSSHESSHEEPLQPFPQLARTKGGQQVDRGPQPALKSRQSVVTLQGSAVVANRT
QAFQEQEQGQGQGQGEPCISSTPRFRKVVRQASVHDSGEEGEA
```

Figure 3

```
          1       10        20        30        40        50        60        70        80        90
          |--------+---------+---------+---------+---------+---------+---------+---------+---------|
    PYST1 DGSPLSNSQPSFPVEILPFLYLGCAKDSTNLDVLEEFGIKYILNVTP-------NLPNLFENAGEFKYKQIPISDHWSQNLSQFFPEAIS
    MKP-7 DGSPVPSSQPAFPVQILPYLYLGCAKDSTNLDVLGKYGIKYILNVTP-------NLPNAFEHGGEFTYKQIPISDHWSQNLSQFFPEAIS
    MKP-4 ATPPPVGLRASFPVQILPNLYLGSARDSANLESLAKLGIRYILNVTP-------NLPNFFEKNGDFHYKQIPISDHWSQNLSRFFPEAIE
     hVH5 LSQPCLPVPSVGLTRILPHLYLGSQKDVLNKDLMTQNGISYVLNASN-------SCPKP-DFICESRFMRVPINDNYCEKLLPWLDKSIE
     PAC1 SDPRVPIYDQGGPVEILPYLYLGSCNHSSDLQGLQACGITAVLNVSA-------SCPNHFE--GLFHYKSIPVEDNQMVEISAWFQEAIS
    MKP-1 SSCSTPLYDQGGPVEILPFLYLGSAYHASRKDMLDALGITALINVSA-------NCPNHFE--GHYQYKSIPVEDNHKADISSWFNEAID
    MKP-2 SSCGTPLHDQGGPVEILPFLYLGSAYHAARRDMLDALGITALLNVSS-------DCPNHFE--GHYQYKCIPVEDNHKADISSWFMEAIE
    MKP-5 NVSYRPAYDQGGPVEILPFLYLGSAYHASKCEFLANLHITALLNVSR-------RTSEACM--THLHYKWIPVEDSHTADISSHFQEAID
      VHR DGSGCYSLPSQPCNEVTPRIYVGNASVAQDIPKLQKLGITHVLNAAEGRSFMHVNTNANFYKDSGITYLGIKANDTQEFNLSAYFERAAD
 AK001790                      MEGTMMMQQRPVLSQQHPSFILNSSPAHSPMAREIDNFYP--ERFTYHNVRLWDEESAQLLPHWKETHR
Consensus ............pveilp.lylgsa........$...gi...LNvs..........pn.f.......%k.!p..D.....ls..f.eai.

          91      100       110       120       130       140       150       160 164
          |--------+---------+---------+---------+---------+---------+---------+---|
    PYST1 FIDEA-RGKNCGVLVHCLAGISRSVTVTVAYLMQKLNLSMNDAYDIVKMKKSNISPNFNFMGQLLDFERTLGLS
    MKP-7 FIDEA-RSKKCGVLVHCLAGISRSVTVTVAYLMQKMNLSLNDAYDFVKRKKSNISPNFNFMGQLLDFERTLGLS
    MKP-4 FIDEA-LSQNCGVLVHCLAGVSRSVTVTVAYLMQKLHLSLNDAYDLVKRKKSNISPNFNFMGQLLDFERSLRLE
     hVH5 FIDKA-KLSSCQVIVHCLAGISRSATIAIAYIMKTMGMSSDDAYRFVKDRRPSISPNFNFLGQLLEYERTLKLL
     PAC1 FIDSV-KNSGGRVLVHCQAGISRSATICLAYLIQSHRVRLDEAFDFVKQRRGVISPNFSFMGQLLQLETQVLCH
    MKP-1 FIDSI-KNAGGRVFVHCQAGISRSATICLAYLMRTNRVKLDEAFEFVKQRRSIISPNFSFMGQLLQFESQVLAP
    MKP-2 YIDAV-KDCRGRVLVHCQAGISRSATICLAYLMMKKRVRLEEAFEFVKQRRSIISPNFSFMGQLLQFESQVLAT
    MKP-5 FIDCV-REKGGKVLVHCEAGISRSPTICMAYLMKTKQFRLKEAFDYIKQRRSMVSPNFGFMGQLLQYESEILPS
      VHR FIDQALAQKNGRVLVHCREGYSRSPTLVIAYLMMRQKMDVKSALSIVRQNRE-IGPNDGFLAQLCQLNDRLAKE
 AK001790 FIEAA-RAQGTHVLVHCKMGVSRSAATVLAYAMKQYECSLEQALRHVQELRPIARPNPGFLRQLQIYQGILTAR
Con en us FI#.a.......VlVHC.aGiSRSat...AYlM.....sl..A...!k..r..isPNf.F$gQLl..#..l...
```

Figure 4

```
   1 CCGGTGCCAG CCCAGGTGCT CGCGGCCTGG CTCCATGGCC CTGGTCACAG TGAGCCGTTC
  61 GCCCCCGGGC AGCGGCGCCT CCACGCCCGT GGGGCCCTGG GACCAGGCGG TCCAGCGAAG
 121 GAGTCGACTC CAGCGAAGGC AGAGCTTTGC GGTGCTCCGT GGGGCTGTCC TGGGACTGCA
 181 GGATGGAGGG GACAATGATG ATGCAGCAGA GGCCAGTTCT GAGCCAACAG AGAAGGCCCC
 241 GAGTGAGGAG GAGCTCCACG GGGACCAGAC AGACTTCGGG CAAGGATCCC AGAGTCCCCA
 301 GAAGCAGGAG GAGCAGAGGC AGCACCTGCA CCTCATGGTA CAGCTGCTGA GGCCGCAGGA
 361 TGACATCCGC CTGGCAGCCC AGCTGGAGGC ACCCCGGCCT CCCCGGCTCC GCTACCTGCT
 421 GGTAGTTTCT ACACGAGAAG GAGAAGGTCT GAGCCAGGAT GAGACGGTCC TCCTGGGCGT
 481 GGATTTCCCT GACAGCAGCT CCCCCAGCTG CACCCTGGGC CTGGTCTTGC CCCTCTGGAG
 541 TGACACCCAG GTGTACTTAG ATGGAGACGG GGGCTTCAGC GTGACGTCTG GTGGGCAAAG
 601 CCGGATCTTC AAGCCCATCT CCATCCAGAC CATGTGGGCC ACACTCCAGG TATTGCACCA
 661 AGCATGTGAG GCAGCTCTAG GCAGCGGCCT TGTACCGGGT GGCAGTGCCC TCACCTGGGC
 721 CAGCCACTAC CAGGAGAGAC TGAACTCCGA ACAGAGCTGC CTCAATGAGT GGACGGCTAT
 781 GGCCGACCTG GAGTCTCTGC GGCCTCCCAG CGCCGAGCCT GGCGGGTCCT CAGAACAGGA
 841 GCAGATGGAG CAGGCGATCC GTGCTGAGCT GTGGAAAGTG TTGGATGTCA GTGACCTGGA
 901 GAGTGTCACT TCCAAAGAGA TCCGCCAGGC TCTGGAGCTG CGCCTGGGGC TCCCCCTCCA
 961 GCAGTACCGT GACTTCATCG ACAACCAGAT GCTGCTGCTG GTGGCACAGC GGGACCGAGC
1021 CTCCCGCATC TTCCCCCACC TCTACCTGGG CTCAGAGTGG AACGCAGCAA ACCTGGAGGA
1081 GCTGCAGAGG AACAGGGTCA CCCACATCTT GAACATGGCC CGGGAGATTG ACAACTTCTA
1141 CCCTGAGCGC TTCACCTACC ACAATGTGCG CCTCTGGGAT GAGGAGTCGG CCCAGCTGCT
1201 GCCGCACTGG AAGGAGACGC ACCGCTTCAT TGAGGCTGCA AGAGCACAGG GCACCCACGT
1261 GCTGGTCCAC TGCAAGATGG GCGTCAGCCG CTCAGCGGCC ACAGTGCTGG CCTATGCCAT
1321 GAAGCAGTAC GAATGCAGCC TGGAGCAGGC CCTGCGCCAC GTGCAGGAGC TCCGGCCCAT
1381 CGCCCGCCCC AACCCTGGCT TCCTGCGCCA GCTGCAGATC TACCAGGGCA TCCTGACGGC
1441 CAGAACCTGA GGGTGGTGGG GAGGAGAAGG TTGTAGGCAT GGAAGAGAGC CAGGCAGCCC
1501 CGAAAGAAGA GCCTGGGCCA CGGCCACGTA TAAACCTCCG AGGGGTCATG AGGTCCATCA
1561 GTCTTCTGGA GCCCTCCTTG GAGCTGGAGA GCACCTCAGA GACCAGTGAC ATGCCAGAGG
1621 TCTTCTCTTC CCACGAGTCT TCACATGAAG AGCCTCTGCA GCCCTTCCCA CAGCTTGCAA
1681 GGACCAAGGG AGGCCAGCAG GTGGACAGGG GGCCTCAGCC TGCCCTGAAG TCCCGCCAGT
1741 CAGTGGTTAC CCTCCAGGGC AGTGCCGTGG TGGCCAACCG GACCCAGGCC TTCCAGGAGC
1801 AGGAGCAGGG GCAGGGGCAG GGGCAGGGAG AGCCCTGCAT TTCCTCTACG CCCAGGTTCC
1861 GGAAGGTGGT GAGACAGGCC AGCGTGCATG ACAGTGGAGA GGAGGGCGAG GCCTGAGCCC
1921 TCACACATGC CCACGCTCCC CTGACACTGA AGAGGATCCA CAACTCCTTG GAGAAACACC
1981 CTCACGTCTG TTGCCGCACA CATTCCTCTC AGCTCCGCCC CATACCCGTC ACTACAGCCT
2041 CACCTCCCAC CCCTGTCACT ACGGCCTCAC CTCCCACCCC TGTCACTACA GCCTCACCTC
2101 CTACAGCCTT AAGTCCCAGG CCCATGTCTG CCTGTCCAAG GGCTCAAGAC TTTCTAACTG
2161 GGATGTGGTA GAGGGACTGA AGGTACCTTT GGGGGCAACA GCACCCTAGT TTCATTCTCA
2221 ACTCTAGCCC TGCACACTCA CCTGTGGCAC GGAATGAAAA CAGAGCTTCC CGTGCAAAAA
2281 GGGTCACGCC TCCCACCCCC GCCCCCTCCC TGCACCTCCT GTCCTCTCCC AGTTCATTCC
2341 TGGAACCAGC CAGGCCAGGC AACCAGTGGC CCCCAAAGGC AGGCAGGATC CTCAGGCCCC
2401 AGCCGCGGGA GGCTGGAAGG GCTGGCAGAT CGCTTCCCTC ATCCACCTCC ACCGGTCCAG
2461 GTCTTTGCTG CTGTCCCCAG ACCTCCTGTG ACACCACGCC AGATCACAGG GCACCAGGCC
2521 AGAGATAGTC TTCTTTTTGT CCTTTCTGGC CTCTGGCTAG TCAGTTTTTC ATAGCCTTAC
2581 AGTATCTGGC TTTGTACTGA GAAATAAAAC ACATTTTC
```

Figure 5

MALVTVSRSPPGSGASTPVGPWDQAVQRRSRLQRRQSFAVLRGAVLGLQDGGDNDDAAEASSEPTEKAPSEEELHGD
QTDFGQGSQSPQKQEEQRQHLHLMVQLLRPQDDIRLAAQLEAPRPPRLRYLLVVSTREGEGLSQDETVLLGVDFPDS
SSPSCTLGLVLPLWSDTQVYLDGDGGFSVTSGGQSRIFKPISIQTMWATLQVLHQACEAALGSGLVPGGSALTWASH
YQERLNSEQSCLNEWTAMADLESLRPPSAEPGGSSEQEQMEQAIRAELWKVLDVSDLESVTSKEIRQALELRLGLPL
QQYRDFIDNQMLLLVAQRDRASRIFPHLYLGSEWNAANLEELQRNRVTHILNMAREIDNFYPERFTYHNVRLWDEES
AQLLPHWKETHRFIEAARAQGTHVLVHCKMGVSRSAATVLAYAMKQYECSLEQALRHVQELRPIARPNPGFLRQLQI
YQGILTART

Figure 6

```
           1       10        20        30        40        50        60        70        80        90       100       110       120       130
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
   DSP-15  MALVTVSRSPPGSGASTPVGPWDQAVQRRSRLQRRQSFAVLRGAV-LGLQDGGDNDDAREASSEPTEKAPSEEELHGDQTDFGQGSQSPQKQEEQRQHLHLMVQLLRPQDDIRLAAQLEAPRPPRLRYLL
 AB036834  QSERRLSTDSTRSSNSTQSNNSDIQLHLQSMFYLLQREDTLKMAVKLESQRSNRTRYLVIASRSCCRSGTSDRRRHRIMRHHSVKVGGSAGTKSSTSPAVPTQRQLSVEQTATEASSKCDKTADKENATA
   DSP-13  MTLSTLARKRKAPLACTCSLGGPDMIPYFSANAVISQNAINQLISESFLTVKGAALFLPRGNGSSTPRISHRRNKHA---------------GDLQQHLQAMFILLRPEDNIRLAVRLESTYQNRTRYMV
   DSP-12
Consensus  ................t............s.............................................h.............................l........a...............

           131    140       150       160       170       180       190       200       210       220       230       240       250       260
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
   DSP-15  VVSTREGEGLSQDETVLLGVDFPDSSSPSCTLGLVLPLWSDTQVYLDGDGGFSVTSGGQSRIFKPISIQTMWATLQVLHQACERALGSGLVPGGSALTWASHYQERLNSEQSCLNEWTAMADLESLRPPS
 AB036834  AGDNKNTSGM--EESCLLGIDCNERT----TIGLVVPILADTTIHLDGDGGFSVKVYEKTHIFKPVSVQAMWSALQTLHKVSKKARENNFYASGPSHDWLSSYERRIESDQSCLNEWNAMDALESRRPPS
   DSP-13  VVSTNGRQDT--EESIVLGMDFSSNDSSTCTMGLVLPLWSDTLIHLDGDGGFSVSTDNRVHIFKPVSVQAMWSALQSLHKACEVARAHNYYPGSLFLTWVSYYESHINSDQSSVNEWNAMQDVQSHRPDS
   DSP-12                                   MVLRLWSDTKIHLDGDGGFSVSTAGRMHIFKPVSVQAMWSALQVLHKACEVARRHNYFPGGVALIWATYYESCISSEQSCINEWNAMQDLESTRPDS
Consensus  .............e...lg.d.........t.g$VlplwsDT.!hLDGDGGFSVst.gr.hIFKP!S!QaMWsaLQvLHkacevAr.hny.pgg.al.WasyY#s.i.S#QSc.NEWnAMqdl#S.RPdS

           261    270       280       290       300       310       320       330       340       350       360       370       380       390
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
   DSP-15  AEP--GGSSEQEQMEQAIRAELWKVLDVSDLESVTSKEIRQALELRLGLPLQQYRDFIDNQMLLLVAQRDRASRIFPHLYLGSEWNAANLEELQRNRVTHILNMAREIDWFYPERFTYHNVRLWDEESAQ
 AB036834  PDAIRNKPPEKEETESVIKMKLKAIMMSVDLDEVTSKYIRGRLEEILDMDLGEYKSFIDAEMLVILGQMDAPTKIFEHVYLGSEWNASNLEELQKNGVRHILNVTREIDNFFPGTFEYFNVRVYDDEKTN
   DSP-13  PALFTDIPTERERTERLIKTKLREIMMQKDLENITSKEIRTELEMQMVCNLREFKEFIDNEMIVILGQMDSPTQIFEHVFLGSEWNASNLEDLQNRGVRYILNVTREIDNFFPGVFEYHNIRVYDEEATD
   DSP-12  PALFVDKPTEGERTERLIKAKLRSIMMSQDLENVTSKEIRNELEKQMNCNLKELKEFIDNEMLLILGQMDKPSLIFDHLYLGSEWNASNLEELQGSGVDYILNVTREIDNFFPGLFAYHNIRVYDEETTD
Consensus  palf.dkptE.ErtErlIkakLr.!$ms.DL#n!TSKeIR.eLE.q$.cnL.#.keFIDn#MllilgQmD.ps.IF.Hl%LGSEWNAsNLE#LQ..gV.yILNvtREIDNF%Pg.F.YhN!RvyD#E.t#

           391    400       410       420       430       440       450       460       470       480       490       500       510       520
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
   DSP-15  LLPHWKETHRFIEAARAQGTHVLVHCKMGVSRSAATVLAYAMKQYECSLEQALRHVQELRPIARPNPGFLRQLQIYQGILTASRQSHVWEQKVGGVSPEEHPAPEVSTPFPPLPPEPEGGGEEKVVGMEE
 AB036834  LLKYWDDTFRYITRAKAEGSKVLVHCKMGVSRSASVVIAYAMKAYQWEFQQALEHVKKRRSCIKPNKNFLNQLETYSGMLDAMKNKEKLQRSKSETNLKSTKDARLLPGSEPTPLI-QALNQAKSKSTGE
   DSP-13  LLAYWNDTYKFISKAKKHGSKCLVHCKMGVSRSASTVIAYAMKEYGWNLDRAYDYVKERRTVTKPNPSFMRQLEEYQGILLASFLGLIHGGRDKPWGEKSTEFESV--DLVSIPGSPSCCNPEKLLHISH
   DSP-12  LLAHWNEAYHFINKAKRNHSKCLVHCKMGVSRSASTVIAYAMKEFGWPLEKAYNYVKQKRSITRPNAGFMRQLSEYEGILDASKQRHNKLWRQQTDSSLQQPVDDPAGPGDFLPETPDGTPESQL-----
Consensus  LLahWn#ty.%I.kAk..gskcLVHCKMGVSRSAstViAYAMKe%gw.l#.Ay.yVk..RsitrPN.gF$rQL.eY.GiLdAskq.h....r....s....p......p...lP..p.g..e.kl.....

           521    530       540       550       560       570       580       590       600       610       620       630       640       650
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
   DSP-15  SQAAPKEEPGPRPRINLRGVMRSISLLEPSLELESTSETSDMPEVFSSHESSHEEPLQPFPQLART-KGGQQVDRGPQPALKSRQSVVTLQGSAVVANRTQAFQEQEQGQGQGQGEPCISSTPRFRKVVR
 AB036834  RGVTPDGEEEDGSRMHRRSIAQKSQ--RRMVRRSSSTSPKTQTAVVTKQQSQSMENLTPERSVAEEPKNMRFPGSNGENYSVTQNQVLHIQKHTPLSVRTRIHDLEAHRADQLPQQPVWTSLTKLITQTS
   DSP-13  PYLTPSIK
   DSP-12  PFLDDAAQPGLGPPLPCCF--------RRLSDPLLPSPEDEAGSLVHLEDPEREALLEEAAPPAEVHRPARQPQQG--SGLCEKDVKKKLEFGSPKGRSGSLLQVEETEREEGLGAGRWGQLP------T
Consensus  p.l.p...pg.gp..............rr.......s........v.......e..l......ae.....rqp..g....l.........l...p........q.ee.....g.g...w..lp.......

           651    660       670       680       690       700       710       720       730       740   746
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+-----|
   DSP-15  QASVHDSGEEGEA
 AB036834  HLGKSVSGSSSGNIDSRRDSSCSDVFSSQVDSVFAKDEGEKRQRRKTHSWTESLGPSGGIVLDPTPQQQKQQSNAILRPRGTRQRELPSRHASWGS
   DSP-13
   DSP-12  QLDQNLLNSENLNNNSKR--SCPN----GMEVGRARPAGWHTPSLPSHS----NWPTSASVVGTTGTRHHTQLIFFYCLLWAPSSHLQGPEGSFTG
Consensus  ql......se..n..s.r..sc............a...g........hs......p....v...t......q..............l.....s...
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